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Research Notes: Amylase and acid phosphatase genotypes of Glycine max, Glycine soja and Neonotonia wightii

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1) Amylase and acid phosphatase genotypes of *Glycine max, Glycine soja* and *Neonotonia wightii*.

Three amylase loci, Am-1, Am-2, and Am-3, have been identified by electrophoresis (Gorman and Kiang, 1978). The activity of amylase at Am-1 and Am-2 is very weak, and that at Am-3 is much stronger. Based on heat lability and chemical reaction, Reiss (1978) concluded Am-1 and Am-2 represent α-amylase and Am-3 β-amylase. The Am-3 locus has four electrophoretic variants, namely, fast (*F*, rf = .51), slow (*S*, rf = .41), null 2 (S^2 slow with weak activity), and null 1 (n_1) (Gorman and Kiang, 1977, 1978; Kiang, 1980, and unpublished data). These four variants appear allelic only with regard to Am-3 with *F* and *S* codominant, S^2 recessive to *F* and *S*, but dominant over n_1 (Kiang, 1980, 1981; Hildebrand and Hymowitz, 1980b).

Soybean-variety-specific acid phosphatase electrophoretic zymograms were reported (Gorman, 1976). No variation was observed for the first and second zymogram bands. The third band (AP-3) displayed three mobility variants, fast (*F*, rf = .53), intermediate (*M*, rf = .48), and slow (*S*, rf = .45) (Gorman and Kiang, 1977). The three variants were found to be controlled by three codominant alleles at a single locus (Gorman, 1976; Hildebrand et al., 1980).

Seeds used in this project were obtained from three sources: 1) R. L. Bernard, USDA, Urbana, IL provided all U.S. named cultivars [*Glycine max* (L.) Merr.], 20 *G. max* introductions each from China, Japan and Korea, 20 accessions each of *G. soja* Sieb. & Zucc. from China, Japan and Korea, and 20 accessions of *Neonotonia wightii* (Arnott) Lackey from Africa; 2) R. G. Palmer, USDA, Ames, IA provided 14 introductions of *G. max* from Belgium, one from Netherlands, and four accessions from Yugoslavia, 15 accessions of *G. soja* from Japan, 18 from USSR and four from Korea; 3) S. Shanmugasundaram, Asian Vegetable Research and Development Center, Taiwan, provided 12 cultivars of *G. max*, 42 accessions of *G. soja* from Korea, and five accessions of *Neonotonia wightii* from Taiwan.

Seeds from each cultivar or accession were examined for amylase and acid phosphatase activity by a polyacrylamide horizontal gel electrophoretic procedure described by Gorman and Kiang (1977). This report does not include acid phosphatase genotypes of named U.S. soybean cultivars since acid phosphatase genotypes of cultivars in the USDA soybean collection have been reported (Hildebrand and Hymowitz, 1980a). For amylase we only report Am-3 genotypes since little variation in Am-1 and Am-2 has been found.

Amylase genotypes of *G. max* named cultivars are presented in Table 1. For acid phosphatase we only report on band 3 (AP-3). Amylase and acid phosphatase genotypes for *G. max* introductions from China, Japan, Korea, and Taiwan are presented in Table 2, those of *G. soja* in Table 3, and those of *N. wightii* in Table 4.

The results clearly indicate the high cultivar purity of soybean seeds. About 0.42% of heterozygous seeds for Am-3 locus, and 0.39% of heterozygous seeds for AP-3 locus were observed in the cultivated soybeans. Gorman (1976) observed 0.37% heterozygous seeds for Am-3 locus among 1361 cultivated soybean seeds. These heterozygous seeds are the products of natural outcrossing.

More heterozygous seeds were observed in *G. soja* seeds, particularly seeds from Japan and Korea. We detected 4.3% of heterozygous seeds for Am-3, and 0.84% for AP-3 from Japanese accessions; 2.5% and 1.85% of heterozygous seeds for Am-3 and AP-3 respectively from Korean accessions. Except for USSR introductions, *G. soja* also showed a higher degree of average polymorphism for Am-3 (13%) and AP-3 (7.1%) compared with *G. max* (Am-3, 1.1%).

We observed a fourth variant at the AP-3 locus in *G. soja* whose mobility is faster than the *F* variant previously reported. We used *VF* to represent

this variant (very fast), and its rf with respect to methyl blue was .57. This fourth variant is probably a codominant allele with the other three codominant alleles since one seed showed a 2-band pattern representing a heterozygote for the *F* and *VF* alleles.

More cultivars in *G. max* are fixed for the *F* allele at the Am-3 locus (86.6%) and for the *M* allele at the AP-3 locus (89.8%). However, in *G. soja* the genotypes are more evenly distributed for *F* and *S* alleles at Am-3 and for *F*, *M*, and *S* alleles at AP-3 locus except for 18 USSR collections, all of which were fixed for the *F* alleles at both the Am-3 and AP-3 loci.

Seeds of *Neonotonia wightii* did not show any amylase activity, except for 2 accessions from South Africa, which showed weak activity with *F* mobility (F^W). The zymograms of acid phosphatase in *N. wightii* are very different from *Glycine max* and *G. soja*. At least two different acid phosphatase zymograms have been observed in *N. wightii* accessions. These have simply been reported as type 1 or type 2. We are currently researching acid phosphatase in other glycine species as well as *N. wightii* and will be reporting the results separately.

Table 1

Amylase genotypes Am-3 of named U.S. soybean cultivars

Cultivar	Maturity group	Am-3	Cultivar	Maturity group	Am-3
A-100	I	*F*	Evans	0	*S*
Acme	00	*S*	Fabulin	IV	*F*
Adams	III	*F*	Fiskeby	00	*F*
Adelphia	III	*F*	Flambeau	00	*F*
Agate	00	*F*	Ford	III	*F*
AK	IV	*F*	Fuji	III	*F*
Aksarben	II	*F*	Funk Delicious	IV	*F*
Altona	00	*F, N*	Funman	II	*F*
Amsoy	II	*S*	Giant Green	I	*F*
Anoka	I	*F*	Gibson	IV	*F*
Aoda	IV	*F*	Goku	II	*F*
Bansei	II	*F*	Goldsoy	0	*F*
Bavender A	III	*F*	Granger	III	*F*
Bavender B	III	*F*	Grant	0	*F*
Bavender C	III	*F*	Green and Black	IV	*F*
Beeson	II	*S*	Guelph	III	*F*
Bethel	IV	*S*	Habaro	I	*F*
Black Eyebrow	II	*F*	Hahto Michigan	IV	*F*
Blackhawk	I	*F*	Hakote	II	*F*

Table 1 - *continued*

Cultivar	Maturity group	Am-3	Cultivar	Maturity group	Am-3
Bombay	I	*F*	Harbinsoy	IV	*F*
Bonus	IV	*S*	Hardome	0	*S*
Boone	IV	*F*	Hark	I	*F*
Burwell	I	*F*	Harly	I	*F*
Calland	III	*F*	Harman	III	*F, S*
Capital	0	*F*	Harosoy	II	*S*
Carlin	IV	*F*	Harosoy 63	II	*S*
Cayuga	I	*F*	Hawkeye	II	*F*
Chestnut	III	S^W	Henry	II	*F*
Chief	IV	*F*	Hidatsa	00	*F*
Chippewa	I	*F*	Higan	IV	*F*
Chusei	III	*F*	Hodgson	I	*F*
Clark	IV	*F*	Hokkaido	IV	*F*
Clay	0	*F*	Hongkong	IV	*F*
Cloud	III	*F*	Hoosier	I	*F*
Columbia	III	*F*	Illington	IV	*F*
Comet	0	*S*	Illini	III	*F*
Corsoy	II	*F*	Imperial	IV	*F*
Crest	00	*S*	Jefferson	IV	*S*
Custer	IV	*F*	Jogun	III	*F*
Cutler	IV	*F*	Kabott	0	*F*
Delmar	IV	*F*	Kagon	I	*F*
Disoy	I	*F*	Kanrich	III	*F*
Dunfield	III	*F*	Kanro	II	*F*
Earlyana	I	*F*	Kanum	II	*F*
Ebony	IV	*S*	Kent	IV	*F*
Elton	I	*F*	Kingston	IV	*F*
Emperor	IV	*F*	Kingway	IV	*F*
Etum	II	*F*	Korean	II	*F*
Kura	III	*F*	Peking	IV	*F*
Lee	VI	*F*	Perry	IV	*F*
Lincoln	III	*F*	Poland Yellow	0	*F*
Lindarin	III	*S*	Pollysoy	IV	*F*
Little Wonder	III	*F*	Portage	00	*S*
Macoupin	IV	*S*	Portugal	I	*F*
Madison	II	*F*	Pridesoy 57	I	*F*
Magna	II	*F*	Prize	II	*F*
Manchu	III	*F*	Protana	II	*F*
Manchu Hudson	II	*F*	Provar	II	*F*
Manchuria	I	*F*	Rampage	I	*F*
Mandarin	I	*S*	Renville	I	*F*
Mandell	III	*F*	Richland	II	*F*
Manitoba Brown	00	*F*	Roe	IV	*F*
Mansoy	III	*F*	Ross	III	*F*
Medium Green	I	*F*	Sac	I	*F*
Mendota	I	*F*	Sangor	IV	*F*
Merit	0	*F, S*	Sato-3	IV	*F*

Table 1 - *Continued*

Cultivar	Maturity group	Am-3	Cultivar	Maturity group	Am-3
Midwest	IV	*F*	Scott	IV	*F*
Miller 67	III	*F*	Seneca	II	*F*
Mingo	III	*F*	Shelby	III	*F*
Minsoy	00	*F*	Shiro	IV	*F*
Monroe	I	*S*	Sioux	00	*F*
Morse	IV	*F*	Sousei	II	*F, S*
Morsoy	00	*F*	Soysota	I	*F*
Mukden	II	*F*	Steele	I	*S*
Norchief	0	*F*	Tastee	II	*F*
Norman	00	*F*	Toku	II	*F*
Norredo	IV	*F*	Tortoise Egg	I	*F*
Norsoy	I	*F*	Traverse	0	*F*
Ogden	IV	*F*	Verde	III	*F*
Ogemaw	00	*F*	Viking	III	*F*
Ontario	I	*F*	Virginia	IV	*F*
Osaya	III	*F*	Waseda	II	*F*
Ottawa	I	*S*	Wayne	III	*F*
Pagoda	00	*S*	Wea	II	*F*
Pando	00	*F*	Willomi	III	*F*
Patoka	IV	*F*	Wilson	IV	*F*
Patterson	IV	*F*	Wolverine	III	*F*
			Yellow Marvel	II	*F*

Table 2

Seed amylase Am-3 and acid phosphatase AP-3 genotypes of soybean (*G. max*) introductions from China, Japan, Korea, Taiwan and Europe

Source		Maturity group	Am-3	AP-3
China	PI 103,080	IV	*S*	*S*
	103,088	III	*F*	*S*
	103,091	IV	*S*	*M*
	103,414	II	*F*	*M*
	103,415	IV	*S*	*S*
	103,419-1	IV	*F*	*F*
	123,577-2	IV	*F*	*M*
	135,589	II	*F*	*S*
	135,590	II	*F*	*M*
	158,765	IV	*F*	*M*
	232,987	II	*F*	*F*
	232,988	II	*F*	*S*
	232,989	II	*F*	*S*

Table 2 - *Continued*

Source		Maturity group	Am-3	AP-3
	232,990	II	*F*	*S*
	232,991	II	*F*	*S*
	253,650A	II	*F*	*M*
	253,650B	II	*F*	*F*
	253,651A	IV	*F*	*M*
	253,651B	IV	*S*	*F*
	253,652A	IV	*F*	*M*
Japan	124,871	IV	*S*	*S*
	181,531	0	*F*	*M*
	181,532	I	*F*	*M*
	181,533	II	*F*	*M*
	181,534	II	*F*	*M*
	181,535	III	*F*	*M*
	181,536	I	*F*	*S*
	181,537	II	*F*	*M*
	181,538	I	*F*	*M*
	181,539	IV	*F*	*M*
	181,540	III	*F*	*M*
	181,541	II	*F*	*M*
	181,542	III	*F*	*M*
	181,548	II	*F*	*M*
	181,549	III	*F*	*M*
	181,550	IV	*F*	*M*
	181,551	IV	*F*	*M*
	181,552	III	*F*	*M*
	181,553	III	*F*	*M*
	181,554	III	*F*	*M*
Korea	157,395	IV	*F*	*M*
	157,396	IV	*F*	*M*
	157,397	III	*F*	*M*
	157,398	IV	*F*	*S*
	157,401	IV	*F*	*F*
	157,402	IV	*F*	*M*
	157,404	IV	*F*	*M*
	157,405	IV	*S*	*M*
	157,408	IV	*F*	*M*
	157,409	IV	*F*	*M*
	157,410	IV	*S*	*F*
	157,414	IV	*F*	*M*
	157,416	III	*F*	*M*
	157,417	IV	*F*	*M*
	157,419	IV	*F*	*M*
	157,421	III	*S*	*S*
	157,424	IV	*S*	*M*
	157,428	IV	*S*	*M*
	157,429	III	*S*	*F*
	157,431	IV	*F*	*M*

Table 2 - *Continued*

Source		Maturity group	Am-3	AP-3
Taiwan	AV* 38		*F*	*M*
	57		*F*	*M*
	62		*F*	*M*
	66		*F*	*M*
	68		*F*	*M*
	69		*F*	*S*
	70		*F*	*M*
	73		*F*	*M*
	215		*F*	*M, S*
	5161		*F*	*S*
	2043		*F*	*M*
	2120		*F*	*S*
Netherlands	PI 132,201	I	N_1	*F*
Belgium	153,274	I	F^1	*M*
	153,275	0	*F*	*M*
	153,277	0	*F*	*M*
	153,278	0	*F*	*M*
	153,279	I	*F*	*M*
	153,282	I	*F*	*M*
	153,283	I	*F*	*M*
	153,284	0	*F*	*M*
	153,289	II	*F*	*S*
	153,292	III	*F*	*S*
	153,300	0	*F*	*M*
	153,304	0	*F*	*M*
	153,305	0	*F*	*M*
	153,306	0	*F*	*F*
Yugoslavia	248,395	0	*F*	*M*
	248,399	0	*F*	*M*
	248,407	I	*F*	*M*
	248,408	0	*F*	*M*

*AV represents Asian Vegetable Research and Development Center Collections.

Table 3

Seed amylase Am-3 and acid phosphatase AP-3 genotypes of *Glycine soja* from China, Japan, Korea and Russia

Source - Area		Maturity	Am-3	AP-3
China - 3	PI 65,549	II	*F*	*F*
- 3	135,624	II	*F*	*F*
- 4	163,453	VII	*F*	-*
- 3	391,587	II	*F*	*F*
- 3	407,288	II	*S*	*F*
- 3	407,289	II	*F*	*F*
- 3	407,290	II	*F*	*S*
- 3	407,291	II	*F*	*S*
- 3	407,292	II	*F*	*S*
- 3	407,293	II	*F*	*S*
- 3	407,294	II	*F*	*F*
- 3	407,295	II	*F*	*F, S*
- 3	407,296	II	*F*	*F*
- 3	407,297	II	*F*	*M*
- 3	407,298	II	*F*	*M*
- 3	407,299	II	*F*	*M*
- 4	407,300	V	*F*	*S*
- 4	407,301	V	*F*	*S*
- 4	407,302	V	*F*	*S*
- 4	407,303	V	*F*	*S*
Japan - 13	203,246	VII	*S*	*M*
- 17	342,434	V	*F*	*M*
- 17	366,122	IV	*S*	*M*
- 15	378,683	VI	*S*	*S*
- 15	387,684A	VI	*F*	*F*
- 15	387,684B	VI	*F*	*M*
- 14	378,685	VI	*S*	*M*
- 14	378,686A	VII	*S*	*F*
- 14	378,686B	VI	*F*	*F*
- 13	378,687A	VI	*F*	-
- 13	378,687B	VII	*S*	-
- 14	378,688	VII	*F*	*M*
- 15	378,689	VI	*S*	-
- 13	378,690	VII	*F*	-
- 13	378,691	VII	*S*	*F*
- 17	378,692	IV	*F*	*F*
- 17	378,693A	VII	*F*	*S*
- 17	378,693B	VII	*F, S*	*M*
- 15	378,694	VI	*S, F*	*M, F*
- 17	378,702	IV	*S*	*F*
-	406,684	?	*S*	*S*
- 16	407,019	V	*F*	*F*

*Dash represents unstudied seeds.

Table 3 - *Continued*

Source - Area			Maturity	Am-3	AP-3
Japan - 16	PI	407,020	V	*F*	*M*
- 16		407,025	V	*S*	*M*
- 16		407,037	V	*F*	*S*
- 16		407,042	V	*F, S*	*F*
- 17		407,048	V	*S*	*F*
- 15		407,054	VI	*F*	*S*
- 15		407,055	VI	*S*	*M*
- 15		407,062	VI	*F*	*F*
- 15		407,080	VI	*S*	*S*
- 15		407,083	VI	*F*	*F*
- 14		407,087	VI	*F*	*F*
- 14		407,107	VI	*F*	*VF*
- 15		407,286	VI	*F*	*M*
	AV*	5005		*F*	*M*
USSR - 1	PI	423,998	00	*F*	*F*
- 1		423,989A	0-00	*F*	*F*
- 1		423,989B	0-00	*F*	*F*
- 1		423,990	0-00	*F*	*F*
- 1		423,991	0-00	*F*	*F*
- 1		423,992	0	*F*	*F*
- 1		423,993	00	*F*	*F*
- 1		423,994	00	*F*	*F*
- 1		423,995	0-00	*F*	*F*
- 1		423,996	00	*F*	*F*
- 1		423,997	00	*F*	*F*
- 1		423,998	00	*F*	*F*
- 1		423,999A	0-00	*F*	*F*
- 1		423,999B	0-00	*F*	*F*
- 1		424,000	00	*F*	*F*
- 1		424,001	00	*F*	*F*
- 1		424,002	00	*F*	*F*
- 1		424,003	00	*F*	*F*
Korea	AV*	3080		*F*	*M*
		3081		*F, S*	*S*
		3083		*F*	-
		3084		*F*	*S*
		3085		*S*	*M*
		3086		*S*	*M*
		3087		*F, S*	*S, VF*
		3089		*F*	-
		3090		*F*	*F*
		3091		*F*	*S*
		3092		*S*	*M*
		3094		*F*	*F*
		3097		*F*	*M*
		3099		*F*	*S*

*AV represents Asian Vegetable Research & Development Center Collections

Table 3 - *Continued*

Source - Area			Maturity	Am-3	AP-3
Korea	AV*	3101		*F*	*S*
		3102		*F*	*M*
		3103		*F*	*F, M, S*
		3104		*F, S*	*S*
		3105		*F, S*	*F, S*
		3106		*F*	*F*
		3107		*F, S*	*F*
		3108		*S*	*VF*
		3109		*F, S*	*S*
		3110		*F*	*S*
		3111		*F*	*M*
		3112		*F*	*F, S*
		3113		*F, S*	*M*
		3114		*F*	*M*
		3120		*F, S*	*F*
		3122		*F*	*S*
		3123		*F, S*	*M*
		3124		*F, S*	*M*
		3125		*F, S*	*M*
		3126		*F, S*	*M*
		3128		*F*	*M*
		3130		*S*	*F*
		3132		*F*	*S*
		3133		*F, S*	*S*
		3136		*F*	*S*
		9055		*F*	-
		9056		*F*	*S*
		9057		*F*	*S*
		9058		*F*	*S*
Korea - 5	PI	339,731	V	*F*	*S*
- 5		339,732	IV	*S*	*S*
- 5		339,733	V	*F*	*M*
- 5		339,735A	IV	*F, S*	*F, S*
- 5		339,735B	IV	*S*	*S*
- 12		339,871A	V	*S*	*F*
- 12		339,871B	V	*F*	*F*
- 11		349,647	V	*S*	*S*
- 11		407,159	V	*F*	*M*
- 11		407,160	V	*S*	*M*
- 11		407,161	V	*F*	*M*
- 11		407,162	IV	*F*	*F*
- 11		407,163	V	*F*	*M*
- 11		407,164	V	*F*	*S*
- 11		407,165	V	*F*	*S*
- 11		407,166	IV	*F*	*M*
- 11		407,167	V	*F*	*M*
- 11		407,168	V	*F*	*M, S*
- 11		407,169	V	*F*	*S*

*AV represents the Asian Vegetable Research & Development Center Collections.

Table 3 - *Continued*

Source - Area		Maturity	Am-3	AP-3
Korea - 11	407,170	V	*F*	*F*
- 5	407,180	V	*S*	*F*
- 5	407,182	IV	*F*	*F*
- 11	407,185	V	*F*	*F*
- 11	407,188	V	*F*	*F*

*AV represents the Asian Vegetable Research & Development Center Collections.

Table 4

Seed amylase Am-3 genotypes of

Neonotonia wightii from Africa and Taiwan

Source		Am-3	A.P.*
Africa	PI 189,613	*N*	-
	224,976	*N*	2
	224,977	F^W	2
	224,978	F^W	2
	224,979	*N*	1
	224,980	*N*	1
	224,981	*N*	1
	230,322	*N*	2
	230,323	*N*	1
	230,324	*N*	2
	230,325	*N*	-
	231,464	*N*	-
	233,148	*N*	-
	234,874	*N*	-
	234,876	*N*	-
	235,287	*N*	-
	245,005	*N*	-
	245,006	*N*	-
	247,677	*N*	1
	255,747	*N*	2
Taiwan	AV 3905	*N*	1
	5154	*N*	1
	5156	*N*	1
	5157	*N*	1
	5158	*N*	1

*A.P. = Acid phosphatase zymogram pattern.

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1) Epistasis and soybean breeding

Epistasis, or non-allelic interaction, may be of considerable importance in the inheritance of quantitative traits in soybeans. Hanson and Weber (1962) and Hanson et al. (1967) used a nested progeny design to partition the genetic variance among homozygous lines into additive and additive x additive (epistatic) components. In each of two populations, approximately 70% of the genetic variance for grain yield was attributable to epistasis. While others (Leffel and Hanson, 1961; Brim and Cockerham, 1961) have given evidence for the predominance of additive variance for soybean yield, the implications for breeders of a large epistatic contribution to yield are worth considering.

A. Line selection. For line selection the reference population is taken to be a collection of homozygous lines extracted at random from a population